

SEQUENCE LISTING

<170> PatentIn Ver. 2.0

<210> 1

<211> 1019

<212> DNA

<213> Homo sapiens

<220>

<223> Description of Sequence: Recombinant
Polynucleotide

<220>

<221> CDS

<222> (16)..(1008)

<400> 1

cccgaattcg ccacc atg atg gat caa gct aga tca gca ttc tct aac ttg 51

Met Met Asp Gln Ala Arg Ser Ala Phe Ser Asn Leu

1

5

10

ttt ggt gga gaa cca ttg tca tat acc cgg ttc agc ctg gct cgg caa 99

Phe Gly Gly Glu Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln

15

20

25

gta gat ggc gat aac agt cat gtg gag atg aaa ctt gct gta gat gaa
147

Val Asp Gly Asp Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu

30

35

40

09030524 401204

gaa gaa aat gct gac aat aac aca aag gcc aat gtc aca aaa cca aaa
195

Glu Glu Asn Ala Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys

45

50

55

60

agg tgt agt gga agt atc tgc tat ggg act att gct gtg atc gtc ttt
243

Arg Cys Ser Gly Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe

65

70

75

ttc ttg att gga ttt atg att ggc tac ttg ggc tat tgt aaa ggg gta
291

Phe Leu Ile Gly Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val

80

85

90

gaa cca aaa act gag gga tcc gag ccc aaa tct tgt gac aaa act cac
339

Glu Pro Lys Thr Glu Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His

95

100

105

aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc
387

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val

110

115

120

ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc
435

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr

125

130

135

140

cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag
483

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu

145

150

155

gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag
531

09830524-101201

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

160

165

170

aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc
579

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser

175

180

185

gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag
627

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

190

195

200

tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc
675

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile

205

210

215

220

tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc
723

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro

225

230

235

cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg
771

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu

240

245

250

gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat
819

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn

255

260

265

ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc
867

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser

T02T03T4250E060

270

275

280

gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg
915

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg

285

290

295

300

tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg
963

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu

305

310

315

cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa
1008

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

320

325

330

tgaagcttgg g
1019

<210> 2

<211> 331

<212> PRT

<213> Homo sapiens

<400> 2

Met Met Asp Gln Ala Arg Ser Ala Phe Ser Asn Leu Phe Gly Gly Glu

1

5

10

15

Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp

20

25

30

FOI 101201 42502524

Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala

35

40

45

Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly

50

55

60

Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly

65

70

75

80

Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr

85

90

95

Glu Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro

100

105

110

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

115

120

125

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

130

135

140

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

145

150

155

160

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

165

170

175

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val

180

185

190

T022197-4290E860

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

195

200

205

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

210

215

220

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp

225

230

235

240

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

245

250

255

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

260

265

270

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

275

280

285

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

290

295

300

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

305

310

315

320

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

325

330

T02T01 "101201" 09830524

<210> 3

<211> 974

<212> DNA

<213> Homo sapiens

<220>

<223> Description of Sequence: Recombinant

Polynucleotide

<220>

<221> CDS

<222> (16)..(963)

<400> 3

cccgaattcg ccacc atg atg gat caa gct aga tca gca ttc tct aac ttg 51

Met Met Asp Gln Ala Arg Ser Ala Phe Ser Asn Leu

1

5

10

ttt ggt gga gaa cca ttg tca tat acc cgg ttc agc ctg gct cgg caa 99

Phe Gly Gly Glu Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln

15

20

25

gta gat ggc gat aac agt cat gtg gag atg aaa ctt gct gta gat gaa
147

Val Asp Gly Asp Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu

30

35

40

gaa gaa aat gct gac aat aac aca aag gcc aat gtc aca aaa cca aaa
195

Glu Glu Asn Ala Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys

45

50

55

60

09830524 101201

agg tgt agt gga agt atc tgc tat ggg act att gct gtg atc gtc ttt
243

Arg Cys Ser Gly Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe

65

70

75

ttc ttg att gga ttt atg att ggc tac ttg ggc tat tgt aaa ggg gta
291

Phe Leu Ile Gly Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val

80

85

90

gaa cca aaa act gag gga tcc gca cct gaa ctc ctg ggg gga ccg tca
339

Glu Pro Lys Thr Glu Gly Ser Ala Pro Glu Leu Leu Gly Gly Pro Ser

95

100

105

gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg
387

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg

110

115

120

acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct
435

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro

125

130

135

140

gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc
483

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala

145

150

155

aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc
531

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

160

165

170

0930534 101201

agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac
579

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr

175

180

185

aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc
627

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

190

195

200

atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg
675

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu

205

210

215

220

ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc
723

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys

225

230

235

ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc
771

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser

240

245

250

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac
819

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp

255

260

265

tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc
867

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser

270

275

280

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct
915

0930524-101201

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
285 290 295 300

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa
963
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
305 310 315

tgaagcttgg g
974

<210> 4

<211> 316

<212> PRT

<213> Homo sapiens

<400> 4

Met Met Asp Gln Ala Arg Ser Ala Phe Ser Asn Leu Phe Gly Gly Glu
1 5 10 15

Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
20 25 30

Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala
35 40 45

Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
50 55 60

Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly

09330524-101201

65

70

75

80

Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr

85

90

95

Glu Gly Ser Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

100

105

110

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

115

120

125

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

130

135

140

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

145

150

155

160

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

165

170

175

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

180

185

190

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

195

200

205

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

210

215

220

09830524 101201

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

225

230

235

240

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

245

250

255

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

260

265

270

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

275

280

285

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

290

295

300

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

305

310

315

<210> 5

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 5

cccggatccg cctccaccaa gggcccatgc gtc

<210> 6

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 6

cccaagcttc atttaccgag agacagggag agg

33

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 7

cccggatccg ccaccatgat ggatcaagct ag

32

<210> 8

<211> 31

<212> DNA

09030524-101201

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 8

cccgattcg ccaaaacgac acccccatct g

31

<210> 9

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

cccaagcttc atttaccagg agagtgggag ag

32

<210> 10

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

09830524-101204
T02T02-4290E860

<400> 10

cccgaattcg ccaccatgat ggatcaagct ag

32

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

tgtccttttg gcctcagttt ttggttctac

30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

ccaaaaactg aggccaaaac gacacccccca

30

<210> 13

0930524-101301

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

cccgaaattcg ccaccatgat ggatcaagct ag

32

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

gtgtgcacac cgctggacag ggatccagag

30

09830524 101201